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BIG DATA PROCESSING AT THE TOMCAT BEAMLINE

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Summary: New advanced technologies at synchrotron facilities are capable to probe time and length-scales previously unachievable, thus involving thousands to millions of measurements at high-resolution to cover cm-sized samples. Within the context of the Human Brain Project, we will discuss our approach for processing and analysing terabytes-sized datasets.

1. INTRODUCTION

With highly brilliant X-rays, sophisticated detector technology and improvements in reconstruction algorithms provided by third generation synchrotron facilities, high-resolution images can be acquired within seconds or few minutes, leading to an impressive amount of data to be stored and analysed. At the TOMCAT beamline of the Swiss Light Source, the acquisition rate reaches 8GB per second of image data [1]. Thus, providing new solutions for post-processing of large amount of data becomes of paramount importance. Such interest is mostly oriented for experiments involving specimens larger than the field of view of the detector, in which a combination of multiple overlapping recordings is needed to enable the visualization of the whole sample volume. In this context, our attention is focused on the reconstruction of the mouse brain micro-vascular network as perfect example of complex sample for which a robust algorithm for image post-processing is mandatory. The algorithm aims to combine (*stitch*) several volumes together and extract valuable quantitative information of the sample, with reduced human interaction and overcoming the computational limits. On top of that, the on-going efforts aim to provide a full reconstruction and an in-depth knowledge of the mouse cerebrovascular system with 1 μm resolution. The entire brain micro-vessel architecture is nowadays not well documented with such high-resolution and with a non-invasive approach despite of its importance in the process of maintaining normal brain function. These new insights of the micro-vascular structure and topology of the mouse brain are essential for better understanding the pathophysiological cerebral processes.

2. EXPERIMENTAL METHOD

Using the X02DA TOMCAT beamline at the Swiss Light Source (Paul Scherrer Institute, Villigen, Switzerland) we have carried out non-destructive studies of the vascular system in the mouse brain. This challenging sample is considered for both testing the algorithm on a complex system and for its importance in neuroscience. The TOMCAT beamline gets photons from a 2.9 T superbend with a critical energy of 11.1 keV. We acquired tomograms using the PCO.Edge camera with high efficiency (QE>70%) coupled with 10× objective and filtered white-beam radiation to further decrease exposure times. This configuration yields a pixel size of 0.65 μm and an effective resolution of about one micron. Filtered white-beam refers to the polychromatic configuration of the beamline where 95% of the total beam power is filtered out of the beam incident on the sample. The bandwidth of the X-ray beam is narrowed down around a mean energy of 25–30 keV. The exposure time in such conditions is set to 30 ms and 1001 projections are acquired while rotating the sample at equiangular steps over 180°. The sample is prepared by intravascular filling with consecutive embedding of the tissue, adopting a protocol suggested by [2]. In order to cover the whole sample volume, local CTs are performed for a total of thousand scans in 30 hours scanning time. In total, 7 TB of datasets are acquired and need to be processed.

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3. RESULTS

In this work, we will discuss our approach for processing terabytes-sized datasets in terms of volume stitching, thus overcoming the limits in the FOV of the detector while preserving image quality (see **Figure 1**). Our method will then be applied in the case of biological samples with particular regards to the mouse cerebral micro-vasculature architecture.
A free tool for image stitching is used on the original reconstructed volume. Most of the image stitching techniques found in literature are performed by using invariant feature detection [3]. The stitching process performs the following steps: a) find the relative position between each pair of adjacent stacks, b) find the optimal displacement between the two stacks and, finally, c) combine all stacks into a single 3D image by replacing the overlapped regions with a blended version of them. However, these methods cannot be directly applied in the case of biological samples due to their complex structure with no clear shape descriptor and, in our specific case, no background because of the local tomography acquisition. As a result, the feature matching fails or the low contrast that characterizes our datasets makes the stitching procedure more prone to the so-called seam artefact [4]. In particular, the process of computing the blending step is quite complex and leads to such artefacts. In this work, we will discuss our approach to address such issues by using the so-called 'puzzle' method [5] and we will present our solution for post-processing terabytes of datasets. At this point, these pioneering efforts are pointing towards new horizons in the investigation of large biological samples with 3D high spatial resolution

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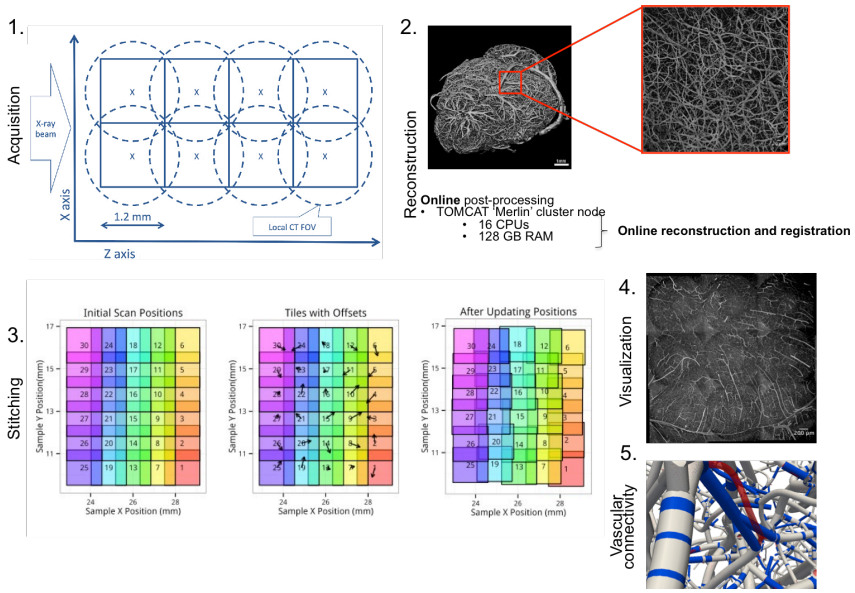

Figure 1: A schematic overview of the project- from image acquisition to processing of TB- sized dataset of the mouse brain